

1 SEQUENCE LISTING

<110> Lee, Se-Jin
McPherron, Alexandra C.

<120> GROWTH DIFFERENTIATION FACTOR RECEPTORS,
AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

<130> JHU1470-2

<150> 09/485,046

<151> 2000-01-31

<150> PCT/US98/15598

<151> 1998-07-28

<150> 60/054,461

<151> 1997-08-01

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 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
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 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu

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260	265	270
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Tyr Pro His Thr His Leu Val	His Gln Ala Asn Pro	Arg Gly Ser Ala
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 Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys
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Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Arg	
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Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr	
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Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln	
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Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val	
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Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro	
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 Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys
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 Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly
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<210> 5

<211> 1131

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1) ... (1128)

<400> 5

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48

att	gct	gct	ggc	cca	gtg	gat	cta	aat	gag	gac	agt	gag	aga	gag	gcg	
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96

Ile	Ala	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asp	Ser	Glu	Arg	Glu	Ala		
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Asn	Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn		
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Thr	Arg	Tyr	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys		
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ctc	cgc	ctg	gaa	aca	gcg	cct	aac	atc	agc	aaa	gat	gct	ata	aga	caa		240
Leu	Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln		
	65				70					75					80		
ctt	ctg	ccc	aga	gcg	cct	cca	ctc	cgg	gaa	ctg	atc	gat	cag	tac	gac		288
Leu	Leu	Pro	Arg	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp		
				85					90					95			
gtc	cag	agg	gat	gac	agc	agt	gac	ggc	tct	ttg	gaa	gat	gac	gat	tat		336
Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr		
			100					105					110				
cac	gct	acc	acg	gaa	aca	atc	att	acc	atg	cct	acc	gag	tct	gac	ttt		384
His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe		
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cta	atg	caa	gcg	gat	gga	aag	ccc	aaa	tgt	tgc	ttt	ttt	aaa	ttt	agc		432
Leu	Met	Gln	Ala	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser		
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tct	aaa	ata	cag	tac	aac	aaa	gtg	gta	aag	gcc	cag	ctg	tgg	ata	tat		480
Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr		
	145				150					155					160		
ctg	aga	gcc	gtc	aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga		528
Leu	Arg	Ala	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg		
				165					170					175			
ctc	atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	acc	gga	atc	cga	tct		576
Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser		
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Leu	Lys	Leu	Asp	Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp		
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Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu		
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Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val		
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acc	ttc	cca	gga	cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc		768
Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val		
			245					250						255			
aaa	gta	aca	gac	aca	ccc	aag	agg	tcc	cgg	aga	gac	ttt	ggg	ctt	gac		816

Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp		
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tgc	gat	gaa	cac	tcc	acg	gaa	tcg	cgg	tgc	tgt	cgc	tac	ccc	ctc	acg		864
Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr		
		275					280					285					
gtc	gat	ttc	gaa	gcc	ttt	gga	tgg	gac	tgg	att	att	gca	ccc	aaa	aga		912
Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg		
	290					295				300							
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Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln		
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aaa	tat	ccg	cat	act	cat	ctt	gtg	cac	caa	gca	aac	ccc	aga	ggc	tcg		1008
Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser		
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gca	ggc	cct	tgc	tgc	acg	cca	aca	aaa	atg	tct	ccc	att	aat	atg	cta		1056
Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu		
		340						345					350				
tat	ttt	aat	ggc	aaa	gaa	caa	ata	ata	tat	ggg	aaa	att	cca	gcc	atg		1104
Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met		
		355					360					365					
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<211> 376

<212> PRT

<213> Rattus norvegicus

<400> 6

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Asn	Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn		
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Thr	Arg	Tyr	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys		
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65				70					75						80		
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		85				90						95					
Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr		
		100				105						110					
His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe		
	115					120						125					
Leu	Met	Gln	Ala	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser		
	130				135						140						
Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr		
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Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	
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Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	
	210					215					220					
Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	
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Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	
			245					250						255		
Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	
			260					265					270			
Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	
	275						280					285				
Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	
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Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	
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Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	
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<211> 1128

<212> DNA

<213> Gallus gallus

<220>

<221> CDS

<222> (1)...(1125)

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gcg	gtt	gat	ccg	gtg	gct	ctg	gat	ggc	agt	agt	cag	ccc	aca	gag	aac	96
Ala	Val	Asp	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
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gct	gaa	aaa	gac	gga	ctg	tgc	aat	gct	tgt	acg	tgg	aga	cag	aat	aca	144
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35					40					45				

aaa	tcc	tcc	aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agc	aaa	ctg	192
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50						55				60					

cgc	ctg	gaa	caa	gca	cct	aac	att	agc	agg	gac	gtt	att	aag	cag	ctt	240
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
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tta	ccc	aaa	gct	cct	cca	ctg	cag	gaa	ctg	att	gat	cag	tat	gat	gtc	288
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				85					90						95	

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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
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gcc	aca	acc	gag	acg	att	atc	aca	atg	cct	acg	gag	tct	gat	ttt	ctt	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				
gta	caa	atg	gag	gga	aaa	cca	aaa	tgt	tgc	ttc	ttt	aag	ttt	agc	tct	432
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
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Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
agg	caa	gtc	caa	aaa	cct	aca	acg	gtg	ttt	gtg	cag	atc	ctg	aga	ctc	528
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
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Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	atc	tgg	cag	agt	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200						205				
aag	aca	gtg	ctg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aat	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
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Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
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Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
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gat	gag	cac	tca	acg	gaa	tcc	cga	tgt	tgt	cgc	tac	ccg	ctg	aca	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
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Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aaa	gcc	aat	tac	tgc	tcc	gga	gaa	tgc	gaa	ttt	gtg	ttt	cta	cag	aaa	960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
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Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
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 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

ttc aat gga aaa gaa caa ata ata tat gga aag ata cca gcc atg gtt 1104
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 355 360 365

gta gat cgt tgc ggg tgc tca tga 1128
 Val Asp Arg Cys Gly Cys Ser
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<210> 8
 <211> 374
 <212> PRT
 <213> Gallus gallus

<400> 8
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 35 40 45
 Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg
 50 55 60
 Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu Leu
 65 70 75 80
 Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val Gln
 85 90 95
 Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala
 100 105 110
 Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Val
 115 120 125
 Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys
 130 135 140
 Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg
 145 150 155 160
 Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile
 165 170 175
 Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys
 180 185 190
 Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys
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 Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile
 210 215 220
 Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr Phe
 225 230 235 240
 Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg Val
 245 250 255
 Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp
 260 265 270
 Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
 Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
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 Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr
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<211> 1128
<212> DNA
<213> Baboon

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn		
			20					25					30				
gtg	gaa	aaa	gag	ggg	ctg	tgt	aat	gca	tgt	act	tgg	aga	caa	aac	act		144
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Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu		
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cgt	ctg	gaa	aca	gct	cct	aac	atc	agc	aaa	gat	gct	ata	aga	caa	ctt		240
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu		
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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His		
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gct	aca	acg	gaa	aca	atc	att	acc	atg	cct	aca	gag	tct	gat	ttt	tta		384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu		
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Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu		
145					150					155					160		
aga	ccc	gtc	gag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc		528

Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu		
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Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu		
			180					185					190				
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			195				200					205					
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Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly		
			210			215					220						
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Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr		
					230				235						240		
ttc	cca	gga	cca	gga	gaa	gat	ggg	ctg	aac	ccc	ttt	tta	gag	gtc	aag		768
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys		
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gta	aca	gac	aca	ccc	aaa	aga	tcc	aga	agg	gat	ttt	ggg	ctt	gac	tgt		816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys		
				260				265					270				
gat	gag	cac	tca	aca	gaa	tcg	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg		864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val		
				275			280					285					
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Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr		
						295					300						
aag	gcc	aac	tac	tgc	tct	gga	gag	tgt	gaa	ttt	gta	ttt	tta	caa	aaa		960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys		
					310					315					320		
tat	cct	cat	act	cat	ctg	gta	cac	caa	gca	aac	ccc	aga	ggg	tca	gca		1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala		
				325					330					335			
ggc	cct	tgc	tgt	act	ccc	aca	aag	atg	tct	cca	att	aac	atg	cta	tat		1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr		
				340				345					350				
ttt	aac	ggc	aaa	gaa	caa	ata	ata	tat	ggg	aaa	att	cca	gcc	atg	gta		1104
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val		
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gta	gac	cgc	tgc	ggg	tgc	tca	tga										1128
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<211> 375

<212> PRT

<213> Baboon

<400> 10

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			20					25					30		
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
		35					40					45			
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55					60				
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
65					70					75					80
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
			100					105					110		
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu
			115				120						125		
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	130					135					140				
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150					155					160
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
				165					170					175	
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			180				185						190		
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		195					200					205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
	210					215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225					230					235					240
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
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Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
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Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			
Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290					295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305					310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340				345					350			
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
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<210> 11

<211> 1128

<212> DNA

<213> Bovine

<220>

<221> CDS

<222> (1)...(1125)

<400> 11

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	
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gtg	gaa	aaa	gag	ggg	ctg	tgt	aat	gca	tgt	ttg	tgg	agg	gaa	aac	act	144
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Glu	Asn	Thr	
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aca	tcg	tca	aga	cta	gaa	gcc	ata	aaa	atc	caa	atc	ctc	agt	aaa	ctt	192
Thr	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					

cgc	ctg	gaa	aca	gct	cct	aac	atc	agc	aaa	gat	gct	atc	aga	caa	ctt	240
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
65					70					75					80	

ttg	ccc	aag	gct	cct	cca	ctc	ctg	gaa	ctg	att	gat	cag	ttc	gat	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val	
				85					90					95		

cag	aga	gat	gcc	agc	agt	gac	ggc	tcc	ttg	gaa	gac	gat	gac	tac	cac	336
Gln	Arg	Asp	Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105					110			

gcc	agg	acg	gaa	acg	gtc	att	acc	atg	ccc	acg	gag	tct	gat	ctt	cta	384
Ala	Arg	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
		115					120					125				

acg	caa	gtg	gaa	gga	aaa	ccc	aaa	tgt	tgc	ttc	ttt	aaa	ttt	agc	tct	432
Thr	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					

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Lys	Ile	Gln	Tyr	Asn	Lys	Leu	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145				150						155					160	

agg	cct	gtc	aag	act	cct	gcg	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	528
Arg	Pro	Val	Lys	Thr	Pro	Ala	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		

atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	act	gga	atc	cga	tct	ctg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			

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Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200						205				

aag	aca	gtg	ttg	cag	aac	tgg	ctc	aaa	caa	cct	gaa	tcc	aac	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					

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225					230					235					240	

ttc	cca	gaa	cca	gga	gaa	gat	gga	ctg	act	ccc	ttt	tta	gaa	gtc	aag	768
Phe	Pro	Glu	Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys	
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gta	aca	gac	aca	cca	aaa	aga	tct	agg	aga	gat	ttt	ggg	ctt	gat	tgt	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
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gat	gaa	cac	tcc	aca	gaa	tct	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
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Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					

aag	gcc	aat	tac	tgc	tct	gga	gaa	tgt	gaa	ttt	gta	ttt	ttg	caa	aag	960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	

tat	cct	cat	acc	cat	ctt	gtg	cac	caa	gca	aac	ccc	aga	ggg	tca	gcc	1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		

ggc	ccc	tgc	tgt	act	cct	aca	aag	atg	tct	cca	att	aat	atg	cta	tat	1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
			340					345					350			

ttt	aat	ggc	gaa	gga	caa	ata	ata	tac	ggg	aag	att	cca	gcc	atg	gta	1104
Phe	Asn	Gly	Glu	Gly	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	
		355				360						365				

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 <212> PRT
 <213> Bovine

<400> 12																
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			20					25					30			
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Glu	Asn	Thr	
		35					40					45				
Thr	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
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Leu	Pro	Lys	Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val	
			85					90					95			
Gln	Arg	Asp	Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100				105					110				
Ala	Arg	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
			115				120					125				

Thr	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
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145					150					155					160
Arg	Pro	Val	Lys	Thr	Pro	Ala	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
			165						170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
			180					185					190		
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		195					200					205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
		210				215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225					230					235					240
Phe	Pro	Glu	Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys
				245					250					255	
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			260					265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			
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		290				295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305					310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
			325						330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
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<211> 1128

<212> DNA

<213> Porcine

<220>

<221> CDS

<222> (1)...(1125)

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	
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gtg	gaa	aaa	gag	ggg	ctg	tgt	aat	gca	tgt	atg	tgg	aga	caa	aac	act	144
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Met	Trp	Arg	Gln	Asn	Thr	
		35					40					45				
aaa	tct	tca	aga	cta	gaa	gcc	ata	aaa	att	caa	atc	ctc	agt	aaa	ctt	192
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					
cgc	ctg	gaa	aca	gct	cct	aac	att	agc	aaa	gat	gct	ata	aga	caa	ctt	240

Arg 65	Leu	Glu	Thr	Ala	Pro 70	Asn	Ile	Ser	Lys	Asp 75	Ala	Ile	Arg	Gln	Leu 80	
ttg	ccc	aaa	gct	cct	cca	ctc	cgg	gaa	ctg	att	gat	cag	tac	gat	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
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cag	aga	gat	gac	agc	agt	gat	ggc	tcc	ttg	gaa	gat	gat	gat	tat	cac	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
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gct	acg	acg	gaa	acg	atc	att	acc	atg	cct	aca	gag	tct	gat	ctt	cta	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
			115				120					125				
atg	caa	gtg	gaa	gga	aaa	ccc	aaa	tgc	tgc	ttc	ttt	aaa	ttt	agc	tct	432
Met	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
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Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
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Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	act	gga	atc	cga	tct	ctg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	att	tgg	cag	agc	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195					200					205				
aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	caa	cct	gaa	tcc	aac	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
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225					230					235					240	
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Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
gta	aca	gac	aca	cca	aaa	aga	tcc	agg	aga	gat	ttt	gga	ctc	gac	tgt	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gat	gag	cac	tca	aca	gaa	tct	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
gat	ttt	gaa	gct	ttt	gga	tgg	gac	tgg	att	att	gca	ccc	aaa	aga	tat	912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aag	gcc	aat	tac	tgc	tct	gga	gag	tgt	gaa	ttt	gta	ttt	tta	caa	aaa	960

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
305 310 315 320

tac cct cac act cat ctt gtg cac caa gca aac ccc aga ggt tca gca 1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
325 330 335

ggc ccc tgc tgt act ccc aca aag atg tct cca atc aat atg cta tat 1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
340 345 350

ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta 1104
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
355 360 365

gta gat cgc tgt ggg tgc tca tga 1128
Val Asp Arg Cys Gly Cys Ser
370 375

<210> 14

<211> 375

<212> PRT

<213> Porcine

<400> 14

Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr
35 40 45

Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
115 120 125

Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160

Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
245 250 255

Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
260 265 270

Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290					295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305					310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
			325					330						335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
		340					345					350			
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
	355					360						365			
Val	Asp	Arg	Cys	Gly	Cys	Ser									
	370					375									

<210> 15

<211> 1128

<212> DNA

<213> Ovine

<220>

<221> CDS

<222> (1)... (1125)

<400> 15

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Met	Gln	Lys	Leu	Gln	Ile	Phe	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Leu	
1				5					10					15		
gtt	gct	ggc	cca	gtg	gat	ctg	aat	gag	aac	agc	gag	cag	aag	gaa	aat	96
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	
			20					25					30			
gtg	gaa	aaa	aag	ggg	ctg	tgt	aat	gca	tgc	ttg	tgg	aga	caa	aac	aat	144
Val	Glu	Lys	Lys	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Gln	Asn	Asn	
		35				40					45					
aaa	tcc	tca	aga	cta	gaa	gcc	ata	aaa	atc	caa	atc	ctc	agt	aag	ctt	192
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					
cgc	ctg	gaa	aca	gct	cct	aac	atc	agc	aaa	gat	gct	ata	aga	caa	ctt	240
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
65					70				75						80	
ttg	ccc	aag	gct	cct	cca	ctc	cgg	gaa	ctg	att	gat	cag	tac	gat	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		
cag	aga	gat	gac	agc	agc	gac	ggc	tcc	ttg	gaa	gac	gat	gac	tac	cac	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105					110			
gtt	acg	acg	gaa	acg	gtc	att	acc	atg	ccc	acg	gag	tct	gat	ctt	cta	384
Val	Thr	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
		115					120					125				
gca	gaa	gtg	caa	gaa	aaa	ccc	aaa	tgt	tgc	ttc	ttt	aaa	ttt	agc	tct	432
Ala	Glu	Val	Gln	Glu	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					

a
 I
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 t
 P
 t
 g
 V
 Q
 g
 A
 D

<210> 16
 <211> 375
 <212> PRT
 <213> Ovine

<400> 16

Met	Gln	Lys	Leu	Gln	Ile	Phe	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Leu
1				5					10					15	
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn
			20					25					30		
Val	Glu	Lys	Lys	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Gln	Asn	Asn
		35					40					45			
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55				60					
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
65					70					75					80
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
				85					90					95	
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
			100					105					110		
Val	Thr	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu
		115					120					125			
Ala	Glu	Val	Gln	Glu	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
	130					135				140					
Lys	Ile	Gln	His	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150					155					160
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
			165						170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
		180					185						190		
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
	195					200					205				
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
	210				215						220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225					230					235					240
Phe	Pro	Glu	Pro	Gly	Glu	Glu	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
			245						250					255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
		260						265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
	275						280					285			
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290				295						300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Leu	Phe	Leu	Gln	Lys
305					310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Lys	Gly	Ser	Ala
			325						330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
		340					345					350			
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Gly	Met	Val
	355						360					365			
Val	Asp	Arg	Cys	Gly	Cys	Ser									
	370					375									

<210> 17
 <211> 1128
 <212> DNA

<213> Meleagris gallopavo

<220>

<221> CDS

<222> (1)...(1125)

<400> 17

atg	caa	aag	cta	gca	gtc	tat	gtt	tat	att	tac	ctg	ttc	atg	cag	att	48
Met	Gln	Lys	Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	
1				5					10					15		

tta	gtt	cat	ccg	gtg	gct	ctt	gat	ggc	agt	agt	cag	ccc	aca	gag	aac	96
Leu	Val	His	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
			20					25					30			

gct	gaa	aaa	gac	gga	ctg	tgc	aat	gct	tgc	acg	tgg	aga	cag	aat	act	144
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35					40					45				

aaa	tcc	tcc	aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agc	aaa	ctg	192
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					

cgc	ctg	gaa	caa	gca	cct	aac	att	agc	agg	gac	gtt	att	aaa	caa	ctt	240
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
65					70				75						80	

tta	ccc	aaa	gct	cct	ccg	ctg	cag	gaa	ctg	att	gat	cag	tat	gac	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		

cag	aga	gac	gac	agt	agc	gat	ggc	tct	ttg	gaa	gac	gat	gac	tat	cat	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100				105						110			

gcc	aca	acc	gaa	acg	att	atc	aca	atg	cct	acg	gag	tct	gat	ttt	ctt	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				

gta	caa	atg	gag	gga	aaa	cca	aaa	tgt	tgc	ttc	ttt	aag	ttt	agc	tct	432
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					

aaa	ata	caa	tat	aac	aaa	gta	gta	aag	gca	caa	tta	tgg	ata	tac	ttg	480
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145				150					155						160	

agg	caa	gtc	caa	aaa	cct	aca	acg	gtg	ttt	gtg	cag	atc	ctg	aga	ctc	528
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165				170					175			

att	aaa	ccc	atg	aaa	gac	ggc	aca	aga	tat	act	gga	att	cga	tct	ttg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180				185						190			

aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	atc	tgg	cag	agt	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200					205					

aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aat	tta	ggc	672
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Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
210						215					220					
atc	gaa	ata	aaa	gct	ttt	gat	gag	aat	gga	cga	gat	ctt	gct	gta	aca	720
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
ttc	cca	gga	cca	ggt	gaa	gat	gga	ctg	aac	cca	ttt	tta	gag	gtc	aga	768
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
				245					250					255		
gtt	aca	gac	aca	cca	aaa	cgg	tcc	cgc	aga	gat	ttt	ggc	ctt	gac	tgc	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gac	gag	cac	tca	acg	gaa	tct	cga	tgt	tgt	cgc	tac	ccg	ctg	aca	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
gat	ttt	gaa	gct	ttt	gga	tgg	gac	tgg	att	ata	gca	cct	aaa	aga	tac	912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aaa	gcc	aat	tac	tgc	tct	gga	gaa	tgt	gaa	ttc	gta	ttt	cta	cag	aaa	960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	
tac	ccg	cac	act	cac	ctg	gta	cac	caa	gca	aat	cca	aga	ggc	tca	gca	1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		
ggc	cct	tgc	tgc	aca	ccc	acc	aag	atg	tcc	cct	ata	aac	atg	ctg	tat	1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
			340					345					350			
ttc	aat	gga	aaa	gaa	caa	ata	ata	tat	gga	aag	ata	cca	gcc	atg	gtt	1104
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	
		355				360						365				
gta	gat	cgt	tgc	ggg	tgc	tca	tga									1128
Val	Asp	Arg	Cys	Gly	Cys	Ser										
	370					375										

<210> 18

<211> 375

<212> PRT

<213> Meleagris gallopavo

<400> 18

Met	Gln	Lys	Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	
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Leu	Val	His	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
			20					25					30			
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35				40						45				
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55				60						
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
65					70				75						80	

Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105					110			
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
	195					200					205					
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu	Ala	Val	Thr	
225					230				235						240	
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
				245					250					255		
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
			340					345					350			
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	
		355					360					365				
Val	Asp	Arg	Cys	Gly	Cys	Ser										
	370					375										

<210> 19

<211> 1125

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (1)...(1122)

<400> 19

atg	cat	ttt	aca	cag	gtt	tta	att	tct	cta	agt	gta	tta	att	gca	tgt	
Met	His	Phe	Thr	Gln	Val	Leu	Ile	Ser	Leu	Ser	Val	Leu	Ile	Ala	Cys	
1				5					10					15		

48

ggt	cca	gtg	ggt	tat	gga	gat	ata	acg	gcg	cac	cag	cag	cct	tcc	aca	
Gly	Pro	Val	Gly	Tyr	Gly	Asp	Ile	Thr	Ala	His	Gln	Gln	Pro	Ser	Thr	
			20					25					30			

96

gcc	acg	gag	gaa	agc	gag	ctg	tgt	tcc	aca	tgt	gag	ttc	aga	caa	cac	
Ala	Thr	Glu	Glu	Ser	Glu	Leu	Cys	Ser	Thr	Cys	Glu	Phe	Arg	Gln	His	
		35					40					45				

144

agc	aag	ctg	atg	aga	ctg	cat	gcc	atc	aag	tcc	caa	att	ctt	agc	aaa	192
Ser	Lys	Leu	Met	Arg	Leu	His	Ala	Ile	Lys	Ser	Gln	Ile	Leu	Ser	Lys	
	50					55					60					
ctc	cga	ctc	aag	cag	gct	cca	aac	atc	agc	cgg	gac	gtg	gtc	aag	cag	240
Leu	Arg	Leu	Lys	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Val	Lys	Gln	
65					70					75					80	
ctg	tta	ccc	aaa	gca	ccg	cct	ttg	caa	caa	ctt	ctg	gat	cag	tac	gat	288
Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Gln	Leu	Leu	Asp	Gln	Tyr	Asp	
				85						90					95	
gtt	tta	gga	gat	gac	agt	aag	gat	gga	gct	gtg	gaa	gag	gac	gat	gaa	336
Val	Leu	Gly	Asp	Asp	Ser	Lys	Asp	Gly	Ala	Val	Glu	Glu	Asp	Asp	Glu	
			100					105					110			
cat	gcc	acc	aca	gag	acc	atc	atg	acc	atg	gcc	aca	gaa	cct	gac	ccc	384
His	Ala	Thr	Thr	Glu	Thr	Ile	Met	Thr	Met	Ala	Thr	Glu	Pro	Asp	Pro	
		115					120					125				
att	gtt	caa	gta	gat	cgg	aaa	ccg	aag	tgt	tgc	ttt	ttc	tcc	ttc	agt	432
Ile	Val	Gln	Val	Asp	Arg	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Ser	Phe	Ser	
	130					135					140					
ccg	aag	atc	caa	gcg	aac	cgg	atc	gta	aga	gcg	cag	ctc	tgg	gtt	cat	480
Pro	Lys	Ile	Gln	Ala	Asn	Arg	Ile	Val	Arg	Ala	Gln	Leu	Trp	Val	His	
145					150					155					160	
ctg	aga	ccg	gcg	gag	gag	gcg	acc	acc	gtc	ttc	tta	cag	ata	tct	cgg	528
Leu	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Thr	Val	Phe	Leu	Gln	Ile	Ser	Arg	
				165					170					175		
ctg	atg	ccc	gtt	aag	gac	gga	gga	aga	cac	cga	ata	cga	tcc	ctg	aaa	576
Leu	Met	Pro	Val	Lys	Asp	Gly	Gly	Arg	His	Arg	Ile	Arg	Ser	Leu	Lys	
			180				185						190			
tatc	gac	gtg	aac	gca	gga	gtc	acg	tct	tgg	cag	agt	ata	gac	gta	aag	624
Ile	Asp	Val	Asn	Ala	Gly	Val	Thr	Ser	Trp	Gln	Ser	Ile	Asp	Val	Lys	
		195					200					205				
cag	gtg	ctc	acg	gtg	tgg	tta	aaa	caa	ccg	gag	acc	aac	cga	ggc	atc	672
Gln	Val	Leu	Thr	Val	Trp	Leu	Lys	Gln	Pro	Glu	Thr	Asn	Arg	Gly	Ile	
	210					215					220					
gag	att	aac	gca	tat	gac	gcg	aag	gga	aac	gac	ttg	gcc	gtc	act	tca	720
Glu	Ile	Asn	Ala	Tyr	Asp	Ala	Lys	Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser	
225					230					235					240	
acc	gag	act	ggg	gag	gat	gga	ctg	ctc	ccc	ttt	atg	gag	gtg	aaa	ata	768
Thr	Glu	Thr	Gly	Glu	Asp	Gly	Leu	Leu	Pro	Phe	Met	Glu	Val	Lys	Ile	
				245					250					255		
tca	gag	ggc	cca	aaa	cga	atc	cgg	agg	gac	tcc	gga	ctg	gac	tgc	gat	816
Ser	Glu	Gly	Pro	Lys	Arg	Ile	Arg	Arg	Asp	Ser	Gly	Leu	Asp	Cys	Asp	
			260					265					270			
gag	aat	tcc	tca	gag	tct	cgc	tgc	tgc	agg	tac	cct	ctc	act	gtg	gac	864
Glu	Asn	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	
		275					280					285				

ttc	gag	gac	ttt	ggc	tgg	gac	tgg	att	att	gct	cca	aaa	cgc	tat	aag	912
Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	
290						295					300					

gcg	aat	tac	tgt	tca	gga	gaa	tgc	gac	tac	atg	tac	ctg	cag	aag	tat	960
Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Asp	Tyr	Met	Tyr	Leu	Gln	Lys	Tyr	
305					310					315					320	

ccc	cac	acc	cat	ctg	gtg	aac	aag	gcc	agt	ccg	aga	gga	acg	gct	ggg	1008
Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala	Ser	Pro	Arg	Gly	Thr	Ala	Gly	
				325					330					335		

ccc	tgc	tgc	act	ccc	acc	aag	atg	tct	ccc	atc	aac	atg	ctt	tac	ttt	1056
Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	
			340					345					350			

aac	ggc	aaa	gag	cag	atc	atc	tac	ggc	aag	atc	cct	tcg	atg	gta	gta	1104
Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ser	Met	Val	Val	
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gac	cgc	tgt	ggc	tgc	tca	tga										1125
Asp	Arg	Cys	Gly	Cys	Ser											
370																

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<211> 374

<212> PRT

<213> Danio rerio

<400> 20

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Gly	Pro	Val	Gly	Tyr	Gly	Asp	Ile	Thr	Ala	His	Gln	Gln	Pro	Ser	Thr	
			20					25					30			
Ala	Thr	Glu	Glu	Ser	Glu	Leu	Cys	Ser	Thr	Cys	Glu	Phe	Arg	Gln	His	
		35					40					45				
Ser	Lys	Leu	Met	Arg	Leu	His	Ala	Ile	Lys	Ser	Gln	Ile	Leu	Ser	Lys	
	50					55					60					
Leu	Arg	Leu	Lys	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Val	Lys	Gln	
65				70					75						80	
Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Gln	Leu	Leu	Asp	Gln	Tyr	Asp	
				85				90						95		
Val	Leu	Gly	Asp	Asp	Ser	Lys	Asp	Gly	Ala	Val	Glu	Glu	Asp	Asp	Glu	
			100					105					110			
His	Ala	Thr	Thr	Glu	Thr	Ile	Met	Thr	Met	Ala	Thr	Glu	Pro	Asp	Pro	
		115					120					125				
Ile	Val	Gln	Val	Asp	Arg	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Ser	Phe	Ser	
	130					135						140				
Pro	Lys	Ile	Gln	Ala	Asn	Arg	Ile	Val	Arg	Ala	Gln	Leu	Trp	Val	His	
145					150					155					160	
Leu	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Thr	Val	Phe	Leu	Gln	Ile	Ser	Arg	
			165						170					175		
Leu	Met	Pro	Val	Lys	Asp	Gly	Gly	Arg	His	Arg	Ile	Arg	Ser	Leu	Lys	
		180						185					190			
Ile	Asp	Val	Asn	Ala	Gly	Val	Thr	Ser	Trp	Gln	Ser	Ile	Asp	Val	Lys	
		195					200					205				
Gln	Val	Leu	Thr	Val	Trp	Leu	Lys	Gln	Pro	Glu	Thr	Asn	Arg	Gly	Ile	
210						215						220				

Glu	Ile	Asn	Ala	Tyr	Asp	Ala	Lys	Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser
225					230					235					240
Thr	Glu	Thr	Gly	Glu	Asp	Gly	Leu	Leu	Pro	Phe	Met	Glu	Val	Lys	Ile
			245						250					255	
Ser	Glu	Gly	Pro	Lys	Arg	Ile	Arg	Arg	Asp	Ser	Gly	Leu	Asp	Cys	Asp
			260						265				270		
Glu	Asn	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp
		275					280					285			
Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys
	290					295					300				
Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Asp	Tyr	Met	Tyr	Leu	Gln	Lys	Tyr
305					310				315					320	
Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala	Ser	Pro	Arg	Gly	Thr	Ala	Gly
			325						330					335	
Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe
			340					345				350			
Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ser	Met	Val	Val
	355						360					365			
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<211> 4

<212> PRT

<213> Artificial Sequence

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<221> VARIANT

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<400> 21

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<211> 4

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<210> 23

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<212> PRT

<213> Eukaryotes

<220>

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<222> (0)...(0)

<223> proteolytic processing site

<400> 23
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<212> DNA
<213> Homo sapiens

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<223> GDF-11

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gtg ctc gcg gcc ccg ctg ctg ctg ggc ttc ctg ctc ctc gcc ctg gag 104
Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Leu Ala Leu Glu
5 10 15

ctg cgg ccc cgg ggg gag gcg gcc gag ggc ccc gcg gcg gcg gcg gcg 152
Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala Ala
20 25 30

gcg gcg gcg gcg gcg gca gcg gcg ggg gtc ggg ggg gag cgc tcc agc 200
Ala Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser Ser
35 40 45

cgg cca gcc ccg tcc gtg gcg ccc gag ccg gac ggc tgc ccc gtg tgc 248
Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val Cys
50 55 60 65

gtt tgg cgg cag cac agc cgc gag ctg cgc cta gag agc atc aag tcg 296
Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys Ser
70 75 80

cag atc ttg agc aaa ctg ccg ctc aag gag gcg ccc aac atc agc cgc 344
Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser Arg
85 90 95

gag gtg gtg aag cag ctg ctg ccc aag gcg ccg ccg ctg cag cag atc 392
Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Ile
100 105 110

ctg gac cta cac gac ttc cag ggc gac gcg ctg cag ccc gag gac ttc 440
Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp Phe
115 120 125

ctg gag gag gac gag tac cac gcc acc acc gag acc gtc att agc atg 488
Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser Met
130 135 140 145

gcc cag gag acg gac cca gca gta cag aca gat ggc agc cct ctc tgc 536
Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu Cys
150 155 160

tgc	cat	ttt	cac	ttc	agc	ccc	aag	gtg	atg	ttc	aca	aag	gta	ctg	aag	584
Cys	His	Phe	His	Phe	Ser	Pro	Lys	Val	Met	Phe	Thr	Lys	Val	Leu	Lys	
			165					170					175			
gcc	cag	ctg	tgg	gtg	tac	cta	cgg	cct	gta	ccc	cgc	cca	gcc	aca	gtc	632
Ala	Gln	Leu	Trp	Val	Tyr	Leu	Arg	Pro	Val	Pro	Arg	Pro	Ala	Thr	Val	
		180					185					190				
tac	ctg	cag	atc	ttg	cga	cta	aaa	ccc	cta	act	ggg	gaa	ggg	acc	gca	680
Tyr	Leu	Gln	Ile	Leu	Arg	Leu	Lys	Pro	Leu	Thr	Gly	Glu	Gly	Thr	Ala	
	195					200					205					
ggg	gga	ggg	ggc	gga	ggc	cgg	cgt	cac	atc	cgt	atc	cgc	tca	ctg	aag	728
Gly	Gly	Gly	Gly	Gly	Gly	Arg	Arg	His	Ile	Arg	Ile	Arg	Ser	Leu	Lys	
210					215					220					225	
att	gag	ctg	cac	tca	cgc	tca	ggc	cat	tgg	cag	agc	atc	gac	ttc	aag	776
Ile	Glu	Leu	His	Ser	Arg	Ser	Gly	His	Trp	Gln	Ser	Ile	Asp	Phe	Lys	
				230					235					240		
caa	gtg	cta	cac	agc	tgg	ttc	cgc	cag	cca	cag	agc	aac	tgg	ggc	atc	824
Gln	Val	Leu	His	Ser	Trp	Phe	Arg	Gln	Pro	Gln	Ser	Asn	Trp	Gly	Ile	
			245					250					255			
gag	atc	aac	gcc	ttt	gat	ccc	agt	ggc	aca	gac	ctg	gct	gtc	acc	tcc	872
Glu	Ile	Asn	Ala	Phe	Asp	Pro	Ser	Gly	Thr	Asp	Leu	Ala	Val	Thr	Ser	
		260					265					270				
ctg	ggg	ccg	gga	gcc	gag	ggg	ctg	cat	cca	ttc	atg	gag	ctt	cga	gtc	920
Leu	Gly	Pro	Gly	Ala	Glu	Gly	Leu	His	Pro	Phe	Met	Glu	Leu	Arg	Val	
	275					280					285					
cta	gag	aac	aca	aaa	cgt	tcc	cgg	cgg	aac	ctg	ggt	ctg	gac	tgc	gac	968
Leu	Glu	Asn	Thr	Lys	Arg	Ser	Arg	Arg	Asn	Leu	Gly	Leu	Asp	Cys	Asp	
290					295					300					305	
gag	cac	tca	agc	gag	tcc	cgc	tgc	tgc	cga	tat	ccc	ctc	aca	gtg	gac	1016
Glu	His	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	
				310					315					320		
ttt	gag	gct	ttc	ggc	tgg	gac	tgg	atc	atc	gca	cct	aag	cgc	tac	aag	1064
Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	
			325					330					335			
gcc	aac	tac	tgc	tcc	ggc	cag	tgc	gag	tac	atg	ttc	atg	caa	aaa	tat	1112
Ala	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Glu	Tyr	Met	Phe	Met	Gln	Lys	Tyr	
		340					345					350				
ccg	cat	acc	cat	ttg	gtg	cag	cag	gcc	aat	cca	aga	ggc	tct	gct	ggg	1160
Pro	His	Thr	His	Leu	Val	Gln	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	
		355				360					365					
ccc	tgt	tgt	acc	ccc	acc	aag	atg	tcc	cca	atc	aac	atg	ctc	tac	ttc	1208
Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	
370					375					380					385	
aat	gac	aag	cag	cag	att	atc	tac	ggc	aag	atc	cct	ggc	atg	gtg	gtg	1256
Asn	Asp	Lys	Gln	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Gly	Met	Val	Val	
				390					395					400		

gat cgc tgt ggc tgc tct taagtgggtc actacaagct gctggagcaa
 Asp Arg Cys Gly Cys Ser
 405

1304

agacttggtg ggtgggtaac ttaacctctt cacagaggat aaaaaatgct tgtgagtatg
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1364

1393

<210> 25

<211> 407

<212> PRT

<213> Homo sapiens

<400> 25

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Glu	Leu	Arg	Pro	Arg	Gly	Glu	Ala	Ala	Glu	Gly	Pro	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Val	Gly	Gly	Glu	Arg	Ser	35	40	45	
Ser	Arg	Pro	Ala	Pro	Ser	Val	Ala	Pro	Glu	Pro	Asp	Gly	Cys	Pro	Val	50	55	60	
Cys	Val	Trp	Arg	Gln	His	Ser	Arg	Glu	Leu	Arg	Leu	Glu	Ser	Ile	Lys	65	70	75	80
Ser	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Lys	Glu	Ala	Pro	Asn	Ile	Ser	85	90	95	
Arg	Glu	Val	Val	Lys	Gln	Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Gln	100	105	110	
Ile	Leu	Asp	Leu	His	Asp	Phe	Gln	Gly	Asp	Ala	Leu	Gln	Pro	Glu	Asp	115	120	125	
Phe	Leu	Glu	Glu	Asp	Glu	Tyr	His	Ala	Thr	Thr	Glu	Thr	Val	Ile	Ser	130	135	140	
Met	Ala	Gln	Glu	Thr	Asp	Pro	Ala	Val	Gln	Thr	Asp	Gly	Ser	Pro	Leu	145	150	155	160
Cys	Cys	His	Phe	His	Phe	Ser	Pro	Lys	Val	Met	Phe	Thr	Lys	Val	Leu	165	170	175	
Lys	Ala	Gln	Leu	Trp	Val	Tyr	Leu	Arg	Pro	Val	Pro	Arg	Pro	Ala	Thr	180	185	190	
Val	Tyr	Leu	Gln	Ile	Leu	Arg	Leu	Lys	Pro	Leu	Thr	Gly	Glu	Gly	Thr	195	200	205	
Ala	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Arg	His	Ile	Arg	Ile	Arg	Ser	Leu	210	215	220	
Lys	Ile	Glu	Leu	His	Ser	Arg	Ser	Gly	His	Trp	Gln	Ser	Ile	Asp	Phe	225	230	235	240
Lys	Gln	Val	Leu	His	Ser	Trp	Phe	Arg	Gln	Pro	Gln	Ser	Asn	Trp	Gly	245	250	255	
Ile	Glu	Ile	Asn	Ala	Phe	Asp	Pro	Ser	Gly	Thr	Asp	Leu	Ala	Val	Thr	260	265	270	
Ser	Leu	Gly	Pro	Gly	Ala	Glu	Gly	Leu	His	Pro	Phe	Met	Glu	Leu	Arg	275	280	285	
Val	Leu	Glu	Asn	Thr	Lys	Arg	Ser	Arg	Arg	Asn	Leu	Gly	Leu	Asp	Cys	290	295	300	
Asp	Glu	His	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	305	310	315	320
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	325	330	335	
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Glu	Tyr	Met	Phe	Met	Gln	Lys	340	345	350	
Tyr	Pro	His	Thr	His	Leu	Val	Gln	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	355	360	365	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr				

1304 1364 1393

$\langle 210 \rangle$	27
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<212> PRT

<213> Salmon-1

<400> 27

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Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser	Ala	Glu	Ala	Gly	Glu	Gly	Leu	Gln
			20					25					30		
Pro	Phe	Met	Glu	Val	Thr	Ile	Ser	Glu	Gly	Pro	Lys	Arg	Ser	Arg	Arg
		35					40					45			
Asp	Ser	Gly	Leu	Asp	Cys	Asp	Glu	Asn	Ser	Pro	Glu	Ser	Arg	Cys	Cys
	50					55					60				
Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile
65					70					75					80
Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
				85					90					95	
Tyr	Met	His	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala
			100					105					110		
Asn	Pro	Arg	Gly	Thr	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
		115					120					125			
Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Arg	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
	130						135					140			
Lys	Ile	Pro	Ser	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser			
145					150					155					

<210> 28

<211> 412

<212> DNA

<213> Salmon-2

<220>

<221> CDS

<222> (2) ... (409)

<400> 28

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	Val	Thr	Ser	Thr	Glu	Ala	Gly	Glu	Gly	Leu	Gln	Pro	Phe	Met	Glu	Val	
1					5					10					15		
aag	att	tcg	gag	ggc	ccg	aag	cgc	tcc	agg	aga	gat	tcg	ggc	ctg	gac		97
Lys	Ile	Ser	Glu	Gly	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Ser	Gly	Leu	Asp		
			20					25					30				
tgt	gat	gag	aac	tcc	ccc	gag	tcc	cgc	tgc	tgc	cgg	tac	ccc	ctc	acg		145
Cys	Asp	Glu	Asn	Ser	Pro	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr		
			35				40					45					
gtg	gac	ttt	gaa	gac	ttt	ggc	tgg	gac	tgg	att	att	gcc	ccc	aag	cgc		193
Val	Asp	Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg		
	50					55					60						
tac	aag	gcc	aac	tac	tgc	tct	ggt	gag	tgc	gag	tac	atg	cac	ctg	cag		241
Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Tyr	Met	His	Leu	Gln		
	65				70				75					80			
aag	tac	ccc	cac	acc	cac	ctg	gtg	aac	aag	gct	aac	cct	cgc	ggc	acc		289
Lys	Tyr	Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala	Asn	Pro	Arg	Gly	Thr		
				85					90					95			
gcg	ggg	ccc	tgc	tgc	acc	ccc	acc	aag	atg	tcc	ccc	atc	aac	atg	ctc		337

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